

AS  
CME-1

17. (Amended) The kit of claim 15, wherein said one of said first pair of PCR primers in step (a)(i) and said one of said second pair of PCR primers in step (a)(ii) also comprise a universal primer binding sequence.

18. (Amended) The kit of claim 15, wherein said one of said first pair of PCR primers in step (a)(i) and said one of said second pair of PCR primers in step (a)(ii) also comprise a unique hybridization tag.

In the Abstract:

Insert the following Abstract, as a separate page, after the last page of claims.

BROAD RANGE PCR AMPLIFICATION TECHNIQUES

Abstract of the Disclosure

Disclosed herein are methods and kits for determining whether a nucleic acid sequence includes a particular allele of a polymorphic sequence. These methods and kits focus on two sets of primers that are specific for an allele and are contacted with a nucleic acid sequence. One primer in each set is complementary to the polymorphic sequence at its 3'-terminal nucleotide and contains one or more mismatches in the five nucleotides adjacent to the 3' terminus. The two sets of primers preferentially amplify the sequence over different concentration ranges. In a preferred embodiment, the methods are used to identify single nucleotide polymorphisms, for example, for genomic mapping purposes.